



PCT10

#6

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/030,549

DATE: 06/04/2002

TIME: 14:58:20

Input Set : A:\Igsln_pct.app

Output Set: N:\CRF3\06042002\J030549.raw

ENTERED

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3 <110> APPLICANT: SOLVAY PHARMACEUTICALS B.V.
5 <120> TITLE OF INVENTION: Novel human G-protein coupled receptor
7 <130> FILE REFERENCE: SPW99.04
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/030,549
C--> 10 <141> CURRENT FILING DATE: 2002-04-26
12 <160> NUMBER OF SEQ ID NOS: 18
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1659
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (36)..(1559)
25 <400> SEQUENCE: 1
26 gcctgcaacc tgctcycacgc cctctggctg ttgcc atg acg tcc acc tgc acc 53
27                               Met Thr Ser Thr Cys Thr
28                               1           5
30 aac agc acg cgc gag agt aac agc agc cac acg tgc atg ccc ctc tcc 101
31 Asn Ser Thr Arg Glu Ser Asn Ser Ser His Thr Cys Met Pro Leu Ser
32           10           15           20
34 aaa atg ccc atc agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg 149
35 Lys Met Pro Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu
36           25           30           35
38 gtt atc ttc ctc gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta 197
39 Val Ile Phe Leu Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu
40           40           45           50
42 gtg ttg cag cgc aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc 245
43 Val Leu Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile
44 55           60           65           70
46 ttt aac ctc ctc gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc 293
47 Phe Asn Leu Leu Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro
48           75           80           85
50 tgg gtg gtg gcc acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac 341
51 Trp Val Val Ala Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His
52           90           95           100
54 ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc 389
55 Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser
56           105           110           115
58 gtc aac acc att gtc ttg gtg tca gtg gat cgc tac ttg tcc atc atc 437
59 Val Asn Thr Ile Val Leu Val Ser Val Asp Arg Tyr Leu Ser Ile Ile
60           120           125           130
62 cac cct ctc tcc tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg 485

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63 His Pro Leu Ser Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu
64 135 140 145 150
66 ctc ctc tat ggc acc tgg att gtg gcc atc ctg cag agc act cct cca 533
67 Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro
68 155 160 165
70 ctc tac ggc tgg ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc 581
71 Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys
72 170 175 180
74 tcc atg atc tgg ggg gcc agc ccc agc tac act att ctc agc gtg gtg 629
75 Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val
76 185 190 195
78 tcc ttc atc gtc att cca ctg att gtc atg att gcc tgc tac tcc gtg 677
79 Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val
80 200 205 210
82 gtg ttc tgt gca gcc cgg agg cag cat gct ctg ctg tac aat gtc aag 725
83 Val Phe Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys
84 215 220 225 230
86 aga cac agc ttg gaa gtg cga gtc aag gac tgt gtg gag aat gag gat 773
87 Arg His Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp
88 235 240 245
90 gaa gag gga gca gag aag aag gag gag ttc cag gat gag agt gag ttt 821
91 Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe
92 250 255 260
94 cgc cgc cag cat gaa ggt gag gtc aag gcc aag gag ggc aga atg gaa 869
95 Arg Arg Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu
96 265 270 275
98 gcc aag gac ggc agc ctg aag gcc aag gaa gga agc acg ggg acc agt 917
99 Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser
100 280 285 290
102 gag agt agt gta gag gcc agg ggc agc gag gag gtc aga gag agc agc 965
103 Glu Ser Ser Val Glu Ala Arg Gly Ser Glu Glu Val Arg Glu Ser Ser
104 295 300 305 310
106 acg gtg gcc agc gac ggc agc atg gag ggt aag gaa ggc agc acc aaa 1013
107 Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys
108 315 320 325
110 gtt gag gag aac agc atg aag gca gac aag ggt cgc aca gag gtc aac 1061
111 Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn
112 330 335 340
114 cag tgc agc att gac ttg ggt gaa gat ggc atg gag ttt ggt gaa gac 1109
115 Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp
116 345 350 355
118 gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag 1157
119 Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu
120 360 365 370
122 agc ctc cca ccc agt cgt cgt aac agc aac agc aac cct cct ctg ccc 1205
123 Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro
124 375 380 385 390
126 agg tgc tac cag tgc aaa gct gct aaa gtg atc ttc atc atc att ttc 1253
127 Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Ile Phe

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Input Set : A:\Igsln_pct.app

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128          395          400          405
130 tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc 1301
131 Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala
132          410          415          420
134 gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata 1349
135 Val Trp Val Asp Val Glu Thr Gln Val Pro Gln Trp Val Ile Thr Ile
136          425          430          435
138 atc atc tgg ctt ttc ttc ctg cag tgc tgc atc cac ccc tat gtc tat 1397
139 Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr
140          440          445          450
142 ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag 1445
143 Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys
144 455          460          465          470
146 aag ttc ttc tgc aag gaa aag ccc ccg aaa gaa gat agc cac cca gac 1493
147 Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp
148          475          480          485
150 ctg ccc gga aca gag ggt ggg act gaa ggc aag att gtc cct tcc tac 1541
151 Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr
152          490          495          500
154 gat tct gct act ttt cct tgaagttagt tctaaggcaa accttgaaaa 1589
155 Asp Ser Ala Thr Phe Pro
156          505
158 tcagtccttc agccacagct atttagagct ttaaaactac caggttcaat cactggttat 1649
160 gctttctgtg 1659
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 508
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169 Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His
170 1 5 10 15
172 Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile
173 20 25 30
175 Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly
176 35 40 45
178 Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
179 50 55 60
181 Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
182 65 70 75 80
184 Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe
185 85 90 95
187 Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His
188 100 105 110
190 Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp
191 115 120 125
193 Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
194 130 135 140
196 Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
197 145 150 155 160

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/030,549

DATE: 06/04/2002

TIME: 14:58:21

Input Set : A:\Igsln_pct.app

Output Set: N:\CRF3\06042002\J030549.raw

```

199 Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
200      165      170      175
202 Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
203      180      185      190
205 Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
206      195      200      205
208 Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala
209      210      215      220
211 Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp
212 225      230      235      240
214 Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
215      245      250      255
217 Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
218      260      265      270
220 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
221      275      280      285
223 Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
224      290      295      300
226 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
227 305      310      315      320
229 Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
230      325      330      335
232 Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly
233      340      345      350
235 Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
236      355      360      365
238 Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
239      370      375      380
241 Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val
242 385      390      395      400
244 Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
245      405      410      415
247 Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro
248      420      425      430
250 Gln Trp Val Ile Thr Ile Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys
251      435      440      445
253 Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu
254      450      455      460
256 Ile Gln Asp Met Leu Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys
257 465      470      475      480
259 Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly
260      485      490      495
262 Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro
263      500      505
267 <210> SEQ ID NO: 3
268 <211> LENGTH: 27
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:

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Input Set : A:\Igsln_pct.app

Output Set: N:\CRF3\06042002\J030549.raw

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273 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
275 <220> FEATURE:
276 <221> NAME/KEY: variation
277 <222> LOCATION: (19)
278 <223> OTHER INFORMATION: Degenerated primers
280 <220> FEATURE:
281 <221> NAME/KEY: variation
282 <222> LOCATION: (22)
283 <223> OTHER INFORMATION: Degenerated primers
285 <220> FEATURE:
286 <221> NAME/KEY: variation
287 <222> LOCATION: (25)
288 <223> OTHER INFORMATION: Degenerated primers
290 <400> SEQUENCE: 3
W--> 291 catcttcgtc gtcggcacng ynggnaa 27
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 26
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
302 <220> FEATURE:
303 <221> NAME/KEY: variation
304 <222> LOCATION: (21)
305 <223> OTHER INFORMATION: Degenerated primers
307 <400> SEQUENCE: 4
W--> 308 ggggtggcaga tggccarrya nckytic 26
311 <210> SEQ ID NO: 5
312 <211> LENGTH: 27
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
319 <220> FEATURE:
320 <221> NAME/KEY: misc_feature
321 <222> LOCATION: (27)
322 <223> OTHER INFORMATION: Modified base : 3'-deoxyadenosine
324 <400> SEQUENCE: 5
325 acggtgggca acacggtgac ggcgtta 27
328 <210> SEQ ID NO: 6
329 <211> LENGTH: 27
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
336 <400> SEQUENCE: 6
337 ccataccta acgactcact atagggc 27
340 <210> SEQ ID NO: 7
341 <211> LENGTH: 23

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/030,549

DATE: 06/04/2002
TIME: 14:58:22

Input Set : A:\Igsln_pct.app
Output Set: N:\CRF3\06042002\J030549.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 19,22,25

Seq#:4; N Pos. 21